Consensus over Activity Driven Networks

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***Abstract*—The problem of self-coordination of a network of dynamical systems toward a common state is often referred to as the consensus problem. In view of its wide range of applications, the consensus problem has been extensively studied in the last decades. However, most of the available results focus on static networks, challenging our mathematical understanding of coordination in temporal networks. In this paper, we study discrete-time stochastic consensus over temporal networks, modeled as activity driven networks. In this paradigm, each node has a specific tendency to create links in the network, measured through an activity potential. Differences in the activity potential of nodes favor the evolution of highly heterogeneous networks, in which some nodes are more involved in the process of information sharing than others. Through stochastic stability theory, we characterize the expected consensus state, which is found to be dominated by low-activity nodes. By further leveraging eigenvalue perturbation techniques, we derive a closed-form expression for the convergence rate in a mean-square sense, which points at a detrimental effect of heterogeneity for large networks. Simulations are conducted to support and illustrate our analytical findings.**

***Index Terms*—Consensus, convergence rate, heterogeneity, mean-square, stability of linear systems, time-varying networks**

I. Introduction

Consensus protocols are a class of distributed algorithms whose goal is to coordinate the units of a network of dynamical systems toward a common state. These protocols find application in an impressively wide range of research domains, including opinion formation, distributed estimation, and multi-vehicle coordination [1]–[3].

Because of this wide range of applications, consensus has received an extensive attention in the last fifteen years. However, most of the research has focused on time-invariant networks [4], and limited efforts have been devoted to time-varying, stochastic networks. Criteria for almost sure convergence of consensus protocols over Erdős-Rényi graphs have been originally presented in [5] and later extended to arbitrary weighted graphs [6]–[10].

Building on these early studies, the literature has brought forward a powerful toolbox of analytical tools that can help elucidate stochastic consensus. For example, a detailed quantification of the asymptotic consensus state is presented in [11], approximate consensus is examined in [12], convergence bounds are established in [13], and systems resilience is studied in [14]. Several authors have investigated criteria for the computation of convergence rates to consensus [15]–[21]. For specific network models, closed-form results have been established, including numerosity-constrained networks [22], linear vectorial models [23], and networks of conspecific agents [24], [25]. Here, we seek to extend the rigorous analysis of network of conspecific agents in [24] to heterogeneous networks of interactions.

We focus on the paradigm of activity driven networks (ADNs), which has emerged as a potent tool to faithfully describe the evolution of several networks of interactions [26]. In ADNs, each node is assigned a fixed parameter, called *activity potential*, which encapsulates its propensity to communicate with its peers. Selecting a range of activity potentials for the nodes in the network allows for elegantly modeling heterogeneity. In the simplest incarnation of ADNs, the activity potential is the probability that a node is *active* in a time unit. The key advantages of ADNs are that i) they allow for reproducing highly heterogeneous networks, in contrast with existing models of time-varying, stochastic networks [26], [27]; and ii) they yield an analytically tractable formulation, which has afforded unprecedented analytical insight into complex problems such as epidemic spreading [28], [29], voting [30], and opinion dynamics [31]. Moreover, many features of real-world networks, such as the presence of community structures [32], [33], heterogeneous nodes' propensity to attract connections [30], state-dependent behavioral changes [34], and memory in the link formation process [35], can be included in the ADN framework, yielding realistic models of social, economical, and technological systems.

Preliminary results on consensus in ADNs, mostly based on computational methods and time-scale separation between the network evolution and the nodes' dynamics, can be found in [36], [37]. Here, we build on these endeavors toward a rigorous mathematical treatment of consensus problems over ADNs. Through stochastic stability theory and eigenvalue perturbation methods, we establish closed-form results for the rate of convergence of the mean-square error dynamics and for the expected consensus state of the network. From the analysis of these expressions, we bring forward surprising evidence on the role of heterogeneity on consensus. Specifically, we determine that low-activity nodes are the most influential in shaping the final state of the network and that the speed of

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convergence could be hindered by the heterogeneity of the nodes' activity.

The main technical contributions of this paper are as follows: i) we extend the analysis of [22] to analytically study the error dynamics in a mean-square sense for consensus problems over ADNs, where the activities of all the units are generally heterogeneous; ii) we demonstrate the application of perturbation techniques to compute a closed-form expression for the convergence rate to consensus, which helps understanding how even modest heterogeneities in the system could impact the effectiveness of the consensus protocol; iii) we analyze the expected consensus state for arbitrary ADNs and perform once more a perturbation analysis to highlight the sensitivity of consensus to heterogeneities in the nodes' activity; and iv) with an eye toward applications of ADNs in real-world problems, we derive a toolbox of asymptotic results for consensus over large networks.

The rest of the paper is organized as follows. In Section II, we introduce the problem statement. In Section III, we recall basic notions of stochastic stability theory for consensus protocols. In Section IV, we analyze the consensus protocol on ADNs and we present our main results. In Section V, we perform an asymptotic analysis of the system for large-scale networks. Section VI concludes the paper and outlines potential avenues of future research.

II. Problem Statement

A. Notation

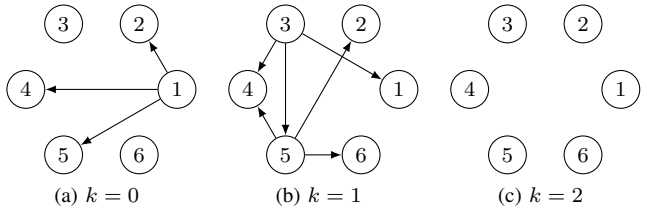
We gather here the notational convention used throughout the paper. $\mathbb{R}$, $\mathbb{R}^+$, and $\mathbb{Z}^+$ are the sets of real, nonnegative real, and nonnegative integer numbers, respectively. $\mathbb{1}$ is the vector of all ones, e_i is a vector with all zeroes but a one in the ith position. Given a vector x, x^T denotes its transpose and $||x||$ its Euclidean norm. Given a matrix M, we denote its spectral radius as $\rho(M)$. I is the identity matrix. Matrices and vectors' dimensions are omitted when not necessary. The operators $\otimes$ and $\oplus$ denote Kronecker product and sum, respectively. The use of Kronecker algebra will often lead us to work with $n^2 \times n^2$ matrices. We write them in n^2 blocks of $n \times n$ matrices. More specifically, given a $n^2 \times n^2$ matrix M, we use four labels to denote the blocks (superscript) and the position of the entry in the block (subscript), as follows:

$$M = \begin{bmatrix} M^{11} & \dots & M^{1n} \\ M^{21} & \dots & M^{2n} \\ \vdots & \ddots & \vdots \\ M^{n1} & \dots & M^{nn} \end{bmatrix} \qquad M^{jh} = \begin{bmatrix} M^{jh}_{11} & \dots & M^{jh}_{1n} \\ M^{jh}_{21} & \dots & M^{jh}_{2n} \\ \vdots & \ddots & \vdots \\ M^{jh}_{n1} & \dots & M^{jh}_{nn} \end{bmatrix}.$$

Thus, M^{jh}_{ik} is the entry in the ith row and kth column of the block in the jth row and hth column of M. Similarly, we write n^2-dimensional vectors as $v = [v^1_1, v^1_2, \dots v^1_n, \dots, v^n_n]$. Expected values of random variables are denoted as $\mathbb{E}[\cdot]$.

B. ADNs' time-evolution

Let $\mathcal{V} = \{1, \dots, n\}$ be a set of $n \geq 3$ nodes connected through a time-varying directed graph $\mathcal{G}_k = (\mathcal{V}, \mathcal{E}_k)$, where $\mathcal{E}_k$ is the time-varying *edge set*, and $k \in \mathbb{Z}^+$ is the discrete time index. The graph $\mathcal{G}_k$ is generated according to a (direct) discrete time ADN [26] with unit time-step and nodes' activity potential given by the vector $a \in (0, 1]^n$. Specifically, at each time step, every node $i \in \mathcal{V}$ activates with probability equal to a_i, independent of the others and the past history of the process. An active node generates $m \leq n-1$ directed links, connecting it with an m-tuple of nodes, selected uniformly among the remaining $n-1$ nodes. Links are oriented from the active node toward the selected nodes and they last for a unit time-step. Then, connections are deleted, the time index updated, and the whole process resumes. Figure 1 depicts the formation of an ADN.



(a) $k = 0$ (b) $k = 1$ (c) $k = 2$

Fig. 1: Exemplary evolution of an ADN. At time $k = 0$, node 1 activates and generates $m = 3$ directed links. At time $k = 1$, nodes 3 and 5 activate, generating 3 links each. At time $k = 2$ none of the nodes activates.

We define the average activity potential and the standard deviation of the activity potential as

$$\bar{a} := \frac{1}{n}\sum_{i=1}^{n} a_i, \qquad \sigma := \sqrt{\frac{1}{n}\sum_{i=1}^{n}(a_i - \bar{a})^2}. \tag{1}$$

The standard deviation σ measures the heterogeneity in the nodes' activity potentials. When $\sigma = 0$, the ADN reduces to the model of conspecific agents proposed in [24]. An alternative way of describing such a heterogeneity consists of separating the average activity, as follows:

$$a_i = \bar{a} + \sigma h_i, \tag{2}$$

where $h \in \mathbb{R}^n$ measures the deviation of each node from the average. Note that, by definition, $\mathbb{1}^T h = 0$ and $||h|| = \sqrt{n}$.

For any discrete time $k \in \mathbb{Z}^+$, we define the adjacency matrix of the time-varying network as $A_k \in \{0, 1\}^{n \times n}$, where $(A_k)_{ij} = 1 \iff (i, j) \in \mathcal{E}_k$, and the Laplacian matrix $L_k := \text{diag}\,(A_k \mathbb{1}) - A_k$, such that

$$(L_k)_{ij} = \begin{cases} -(A_k)_{ij} & \text{if } i \neq j \\ \sum_{h \neq i}(A_k)_{ih} & \text{if } i = j. \end{cases} \tag{3}$$

By construction, matrices L_k's are a sequence of independent and identically distributed (i.i.d.) random variables; we refer to L as their common random variable.

C. Consensus over ADNs

The nodes' dynamics are defined as follows. Each node $i \in \mathcal{V}$ has a continuous state $x_i(k) \in \mathbb{R}$, which evolves according to a discrete-time consensus protocol (see [3], Section 3), starting from an initial condition $x_0 \in \mathbb{R}^n$. At each time step, every node updates its state by averaging with

the nodes with which it is temporarily connected. Specifically, a generic node $i \in \mathcal{V}$ updates its state to

$$x_i(k+1) = (1 - \varepsilon m)x_i(k) + \varepsilon \sum_{j \in \mathcal{V}} A_{ij} x_j(k), \qquad (4)$$

if $(L_k)_{ii} = m$, while it remains $c_i(k+1) = x_i(k)$, if $(L_k)_{ii} = 0$. The parameter $\varepsilon > 0$ is used to capture the nodes' tendency to compromise. Specifically, ε is the weight that each node assigns to the state of its neighbors during the update process: the larger is ε, the more a node will favor the average state of the neighbors against its own during the updating process. Hence, consensus dynamics is described by the following time-varying linear system:

$$x(k+1) = (I - \varepsilon L_k)x(k) := P_k x(k), \qquad (5)$$

with initial condition $x(0) = x_0$, where the *consensus matrices* P_k's are a sequence of i.i.d. random variables. In general, P_k's are nonsymmetric and their entries are not required to be nonnegative. We say that the consensus protocol converges to a *consensus state* $\bar{x}$ if $\lim_{k\to\infty} x(k) = \bar{x}\mathbb{1}$, that is, all nodes asymptotically attain the same state. Given that (5) is a stochastic system, convergence must be defined in a stochastic sense [38].

From the literature, almost sure convergence (that is, convergence with probability 1) can be established for $\varepsilon < 1/m$, which guarantees that P_k's are nonnegative, and thus stochastic (see, for example, [3], Section 3). Here, we focus on mean-square convergence, which places no constraint on the selection of ε and guarantees almost sure convergence in our setting (see, for example, [13], [38], [39]). Through the lens of mean-square convergence, one can aim at an analytical study of the rate of convergence of the protocol, which is known to be unfeasible in an almost sure sense, beyond a few low-dimensional toy problems where one can compute the largest sample-path Lyapunov exponent (more details can be found in [40]–[42]).

III. Preliminary Results

Here, we review some basic notions of stochastic stability and key properties of stochastic consensus protocols. First, we introduce the *agreement subspace* $\mathcal{A} = \{v \in \mathbb{R}^n : v = \mu\mathbb{1}, \mu \in \mathbb{R}\}$ and its orthogonal complement $\mathcal{A}^\perp = \{v \in \mathbb{R}^n : v^T u = 0, \forall\, u \in \mathcal{A}\}$, called the *disagreement subspace*. To study the convergence of the consensus protocol to a consensus state, the dynamics $x(k)$ is projected onto the disagreement subspace, by means of a matrix $Q \in \mathbb{R}^{n\times(n-1)}$, such that $Q^T\mathbb{1} = 0$ and $Q^TQ = I$ (see, for example, [22]). The dynamics of the *disagreement vector* $\xi(k) = Q^T x(k)$ is

$$\xi(k+1) = Q^T P_k Q \xi(k) = \tilde{P}_k \xi(k), \qquad (6)$$

with initial condition $\xi(0) = \xi_0 = Q^T x_0$. The mean-square stability analysis of the disagreement vector permits to formalize a necessary and sufficient condition for mean-square consentability for a consensus protocol, which is defined as follows.

Definition 1 (Definition 2 from [43])**.** *Consensus protocol* (5) *is said to be mean-square consentable if for any* $i \neq j$, $|x_i(k) - x_j(k)| \to 0$ *in mean square sense,* $\forall\, \xi_0 \in \mathbb{R}^{n-1}$.

The necessary and sufficient condition for mean-square consentability based on the disagreement vector is the following.

Proposition 1 (Section III.B from [22])**.** *Consensus protocol* (5) *is mean-square consentable if and only if the disagreement dynamics* (6) *is mean-square asymptotically stable, that is, if* $\lim_{k\to\infty} \mathbb{E}[||\xi(k)||^2] = 0$, $\forall\, \xi_0 \in \mathbb{R}^{n-1}$.

For a linear system like (5), whose matrices P_k's are i.i.d., it has been shown that mean-square convergence implies almost sure convergence; details can be found in Proposition 4.3 from [39] and in Section 2 of [38], for the more general case of state matrices from an ergodic Markov chain. Hence, in our setting, mean-square consentability implies almost sure convergence to consensus. In order to quantify the speed of convergence of the protocol toward consensus, we use the asymptotic convergence factor of the disagreement dynamics [13], that is,

$$r := \sup_{||\xi_0||\neq 0} \lim_{k\to\infty} \left(\frac{\mathbb{E}[||\xi(k)||^2]}{||\xi_0||^2} \right)^{1/k}. \qquad (7)$$

The smaller the convergence factor, the faster the convergence of the dynamics is. In [44], it is proved that $r < 1$ is a necessary and sufficient condition for mean-square consentability. The following result establishes an easy-to-use expression for the convergence factor.

Proposition 2 (Proposition 1 and Theorem 1 from [22])**.** *Protocol* (5) *is mean-square consentable if and only if its convergence factor* $r < 1$. *The convergence factor is equal to the spectral radius* $\rho(G)$ *of the second-order consensus matrix*

$$G = (R \otimes R)\left(I - \varepsilon\mathbb{E}[L] \oplus \mathbb{E}[L] + \varepsilon^2 \mathbb{E}[L \otimes L]\right), \qquad (8)$$

where $R = QQ^T = I - \frac{1}{n}\mathbb{1}\mathbb{1}^T$.

For a mean-square consentable protocol, where convergence to consensus is guaranteed almost surely, the expected consensus state $\mathbb{E}[\bar{x}]$ can be computed using the following result, which is indeed valid for the less restrictive case of almost sure consensus.

Proposition 3. *Let protocol* (5) *be mean-square consentable. Then, the expected consensus state is* $\mathbb{E}[\bar{x}] = \pi^T x_0$, *where* π *is the left eigenvector associated with the null eigenvalue of* $\mathbb{E}[L]$.

Proof. By using (5) recursively and computing the expected value, we obtain

$$\mathbb{E}[x(k)] = \mathbb{E}\left[\prod_{h=0}^{k-1} P_k\right] x(0) = \mathbb{E}[P]^k x_0, \qquad (9)$$

where the last equality holds since P_k's are i.i.d. random variables with common random variable $P = I - \varepsilon L$. Hence, $\mathbb{E}[x(k)]$ evolves as a time-invariant deterministic protocol with consensus matrix $\mathbb{E}[P]$. According to Theorem 2.2 from [3], since $\mathbb{E}[x(k)] \to \bar{x}\mathbb{1}$, then $\mathbb{E}[P]^k \to \mathbb{1}\mu^T$. By expressing $\mathbb{E}[P]$ in terms of its Jordan canonical form, we conclude that μ is the

left eigenvector associated with the unit eigenvalue of $\mathbb{E}[P]$, which, in turn, coincides with the left eigenvector associated with the null eigenvalue of $\mathbb{E}[L]$. □

IV. Analysis of the Consensus Protocol

The analysis of the consensus protocol on ADNs is carried out with two objectives. First, we compute the convergence factor of the consensus protocol by using an eigenvalue perturbation argument. This closed-form result enables us to derive a sufficient condition for almost sure convergence, and it unveils a potentially adversary effect of heterogeneity on the convergence speed of the protocol. Then, we study the effect of the nodes' activity on the formation of the consensus state, under the premise of mean-square consentability. Specifically, we demonstrate that nodes with low activity influence the most the expected consensus state.

A. Convergence Speed to Consensus

We examine consentability of (5) by computing the convergence factor r, which is equal to the spectral radius of matrix G in (8), according to Proposition 2. The exact computation of $\rho(G)$ for an arbitrary set of activities a_i's does not seem feasible when the activity potentials are heterogeneous, due to the nontrivial structure of the two matrices $\mathbb{E}[L] \oplus \mathbb{E}[L]$ and $\mathbb{E}[L \otimes L]$ in Proposition 2.

To address this issue, we study the effect of heterogeneity through a perturbation argument. Specifically, the expression for the activity potentials in (2) enables us to separate the effect of the average activity potential (which is studied through the paradigm of conspecific agents [22]) from the heterogeneity in the activity potential (which acts as a perturbation factor). Hence, we write matrix $G = G_0 + \sigma G_1 + O(\sigma^2)$, where G_0 is the second-order consensus matrix for an ADN with homogeneous activity potentials equal to $\bar{a}$, whose spectrum is given in [24]. Such a perturbation analysis allows for computing the convergence rate of consensus on ADNs in closed-form, up to an error of the order of σ^2, shedding light on how a modest heterogeneity in the activity of the nodes influences the consensus dynamics.

To prove our main result, the following intermediate steps are carried out. In Lemma 1, we recall the computation of the spectral radius of the unperturbed component of matrix G, that is, $\rho(G_0)$, from [24]. Then, the first-order perturbation G_1 is evaluated in Lemma 2. In Lemma 3, we reckon that the first-order perturbation of the spectral radius is null. This evidence calls for the evaluation of the first-order perturbation of the associated eigenvector, in Lemma 4, which allows for the computation of the second-order perturbation of the spectral radius. Theorem 1 consolidates these findings into our main result.

Lemma 1 (Theorem 1 from [24])**.** *Under the assumptions $m \geq 1$, $\bar{a} > 0$, and $\varepsilon > 0$, the spectral radius $\rho_0 := \rho(G_0)$ is associated with a simple eigenvalue, equal to*

$$\rho_0 = 1 - \varepsilon \frac{2\bar{a}mn}{n-1} + \varepsilon^2 \bar{a} m \left[\frac{nm\bar{a}}{(n-1)^2} + m + 1 \right], \qquad (10)$$

and its corresponding eigenvector is

$$u_0 = \frac{1}{\sqrt{n-1}} \mathrm{vec}(R). \qquad (11)$$

Matrix G_0 has at most three other real eigenvalues,

$$\begin{aligned} \lambda^{(1)} &= 0, \\ \lambda^{(2)} &= 1 - \varepsilon \frac{2\bar{a}mn}{n-1} + \varepsilon^2 \bar{a} m \left[2\frac{nm\bar{a}}{(n-1)^2} + m - \frac{1}{n-1} \right], \\ \lambda^{(3)} &= \left(1 - \frac{\varepsilon m \bar{a} n}{n-1} \right)^2, \end{aligned} \qquad (12)$$

whose corresponding eigenspaces are, respectively,

$$\begin{aligned} \Gamma^{(1)} &= \left\{ v \in \mathbb{R}^{n^2} : v = w \otimes \mathbb{1}, \text{ or } v = \mathbb{1} \otimes w, \, w \in \mathbb{R}^n \right\} \\ \Gamma^{(2)} &= \left\{ \begin{array}{l} v \in \mathbb{R}^{n^2} : v_i = b_i R e_i - \dfrac{1}{n} \displaystyle\sum_{j \in \mathcal{V}} b_j R e_j, \\ \mathbb{1}^T b = 0, \, b \in \mathbb{R}^n \end{array} \right\} \\ \Gamma^{(3)} &= \left\{ v \in \mathbb{R}^{n^2} : \sum v_i = 0, \, v_i^T \mathbb{1} = 0, \, e_i^T v_i = 0 \right\}, \end{aligned} \qquad (13)$$

where the notation $v^T = [v_1^T, \ldots, v_n^T]$ is used. The dimensions of $\Gamma^{(1)}$, $\Gamma^{(2)}$, and $\Gamma^{(3)}$ are $2n+1, n-1, n^2-3n-1$, respectively, and these spaces are mutually orthogonal and to the span of u_0.

Lemma 2. *The first-order perturbation associated with the activity's heterogeneity is $G_1 = (R \otimes R)M$, where*

$$\begin{aligned} M^{jj} = \; & -\varepsilon \left[\frac{n}{n-1} m \mathrm{diag}\,(h) R + m h_j I \right] \\ & + \varepsilon^2 \frac{nm^2}{n-1} h_j \left[\bar{a}(R - e_j (Re_j)^T) + e_j (Re_j)^T \right] \\ & + \varepsilon^2 \frac{nm^2}{n-1} \bar{a} \left[\mathrm{diag}\,(h)(R - e_j (Re_j)^T) \right], \\ M^{jh} = \; & \varepsilon \frac{m}{n-1} h_j I + \varepsilon^2 \frac{m}{n-1} h_j e_j [e_h^T - m e_j^T] \\ & - \varepsilon^2 \frac{nm^2}{(n-1)^2} \bar{a} \left[\mathrm{diag}\,(h)(R - e_j (Re_j)^T) \right] \\ & + \varepsilon^2 \frac{m(m-1)}{(n-1)(n-2)} h_j e_j \left[\mathbb{1}^T - e_h^T - e_j^T \right] \\ & - \varepsilon^2 \frac{nm^2}{(n-1)^2} \bar{a} h_j (R - e_j (Re_j)^T), \text{ for } h \neq j. \end{aligned} \qquad (14)$$

Proof. With respect to its ith row, the random variable L is defined as follows:

- with probability a_i, $L_{ii} = m$ and m off-diagonal entries, chosen uniformly at random, are equal to -1, while the others are equal to 0; and
- with probability $1 - a_i$, all the entries are equal to 0.

Therefore, we find $\mathbb{E}[L] = \frac{n}{n-1} m \,\mathrm{diag}(a) R$. Through a cumbersome, counting argument, we can compute the two matrices $\mathbb{E}[L] \oplus \mathbb{E}[L]$ and $\mathbb{E}[L \otimes L]$. Their expressions, block-wise, are

$$\begin{aligned} (\mathbb{E}[L] \oplus \mathbb{E}[L])^{jj} &= \frac{n}{n-1} m \mathrm{diag}(a) R + m a_j I, \\ (\mathbb{E}[L] \oplus \mathbb{E}[L])^{jh} &= -\frac{1}{n-1} m a_j I, \end{aligned} \qquad (15)$$

$$
\begin{aligned}
(\mathbb{E}[L\otimes L])^{jj} &= \frac{nm^2}{n-1}a_j\left[\text{diag}(a)(R-e_j(Re_j)^T)\right.\\
&\quad \left.+e_j(Re_j)^T\right],\\
(\mathbb{E}[L\otimes L])^{jh} &= -\frac{nm^2}{(n-1)^2}a_j\left[\text{diag}(a)(R-e_j(Re_j)^T)\right]\\
&\quad +\frac{m(m-1)}{(n-1)(n-2)}a_je_j\left[\mathbb{1}^T-e_h^T-e_j^T\right]\\
&\quad +\frac{m}{n-1}a_je_j[e_h^T-me_j^T].
\end{aligned}
\tag{16}
$$

The expression for M is obtained by combining the matrices above according to (8), expressing the activity potentials through (2), and collecting all the terms in σ. □

Remark 1. *While the unperturbed matrix G_0 is symmetric, the first-order perturbation matrix G_1 is in general not symmetric.*

Next, we recall the following result from second-order perturbation theory of simple eigenvalues, which is often used in quantum mechanics [45], applied to the spectral radius of G.

Proposition 4 (From [45], Chapter 6.1)**.** *The spectral radius $\rho(G)$ can be written as $\rho(G)=\rho_0+\sigma\rho_1+\sigma^2\rho_2+O(\sigma^3)$. The first-order perturbation is given in terms of u_0 and G_1 as*

$$\rho_1 = u_0^TG_1u_0. \tag{17}$$

The second-order correction requires knowledge of the first-order perturbation to the eigenvector associated with the spectral radius. Specifically,

$$\rho_2 = u_0^TG_1u_1, \quad \textit{with} \quad u_1=\sum_{i=2}^{n^2}\frac{v_i^TG_1u_0}{\rho_0-\lambda_i}v_i, \tag{18}$$

where $\lambda_2,\dots,\lambda_{n^2}$ are the n^2-1 eigenvalues of G_0 in (12)*, counted with their multiplicity, and $v_2,\dots,v_{n^2}$ are their corresponding eigenvectors in the eigenspaces in* (13)*.*

Vector u_1 represents the first-order perturbation to the eigenvector associated with the spectral radius of G, that is, $u=u_0+\sigma u_1+O(\sigma^2)$, with u_0 defined in (11). While in many practical applications it is sufficient to retain a first-order perturbation to gain insight into the role of a critical parameter [46], consensus over ADNs requires the study of second-order corrections. In fact, the next claim shows that $\rho_1=0$.

Lemma 3. *Under the assumptions $m\geq 1$, $\bar{a}>0$, and $\varepsilon>0$, the first-order perturbation correction to the spectral radius $\rho(G)$ is $\rho_1=0$.*

Proof. Based on Proposition 4, we compute $\rho_1=u_0^TG_1u_0$. First, recalling (11), we define the vector $\tilde{y}:=Mu_0$, that is,

$$
\begin{aligned}
\tilde{y}_i^j &= \sum_{h,k\in\mathcal{V}}M_{ik}^{jh}(u_0)_{kh}=\frac{1}{\sqrt{n-1}}\sum_{h,k\in\mathcal{V}}M_{ik}^{jh}R_{kh}=\\
&= \frac{1}{\sqrt{n-1}}\left[\frac{n-1}{n}\sum_{h\in\mathcal{V}}M_{ih}^{jh}-\frac{1}{n}\sum_{h\in\mathcal{V},k\neq h}M_{ik}^{jh}\right],
\end{aligned}
\tag{19}
$$

which can be computed using the explicit expression of M in Lemma 2. Details can be found in the Appendix. Then, we evaluate $y=(R\otimes R)\tilde{y}$ entry-wise, as

$$y_i^i=\frac{(n-1)^2}{n^2}\tilde{y}_i^i-\frac{n-1}{n^2}\left(\sum_{h\neq i}\tilde{y}_i^h+\sum_{k\neq i}\tilde{y}_k^i\right)+\frac{1}{n^2}\sum_{h,k\neq i}\tilde{y}_k^h, \tag{20}$$

and, similarly, for the off-diagonal elements. Explicit computations of vectors $\tilde{y}$ and y are cumbersome, but they follow directly from the expression of M. Details are summarized in the Appendix. We present the final result, that is,

$$y_i^j=\begin{cases}\dfrac{n-2}{n}\dfrac{1}{\sqrt{n-1}}\varepsilon m\gamma h_i & \text{if } i=j\\ -\dfrac{1}{n\sqrt{(n-1)}}\varepsilon m\gamma(h_i+h_j) & \text{if } i\neq j,\end{cases} \tag{21}$$

with

$$\gamma:=\frac{2n}{(n-1)^2}\varepsilon m\bar{a}-\frac{2n}{n-1}+\varepsilon m+\varepsilon. \tag{22}$$

In a more compact form, we write

$$y=\sqrt{\frac{n-2}{n-1}}\varepsilon m\gamma q, \tag{23}$$

where the unit-norm vector $q^T=[q_1^T,\dots,q_n^T]$ is

$$q_i:=\sqrt{\frac{n}{n-2}}h_iRe_i-\frac{1}{\sqrt{n(n-2)}}\sum_{j\in\mathcal{V}}h_jRe_j \tag{24}$$

From (13), we note that $y\in\Gamma^{(2)}$. Since eigenspaces are mutually orthogonal, y is orthogonal to u_0. Hence, (17) implies $\rho_1=u_0^TG_1u_0=u_0^Ty=0$. □

Thus, a first-order perturbation is not sufficient to elucidate the role of the heterogeneity in the nodes' activity on the rate of convergence of the protocol. We use the spectral characterization of G_0 in Lemma 1 to prove the following statement.

Lemma 4. *Under the assumptions $m\geq 1$, $\bar{a}>0$, and $\varepsilon>0$, the first-order perturbation correction to the eigenvector of G associated with its spectral radius is*

$$u_1=\frac{\sqrt{(n-2)(n-1)}}{\varepsilon\bar{a}n\left(1-\dfrac{m\bar{a}}{n-1}\right)}\gamma q, \tag{25}$$

where vector q is defined in (24) *and parameter γ in* (22)*.*

Proof. We split the summation of u_1 in (18) into three terms, one for each eigenspace of G_0, such that

$$u_1=\left[\frac{1}{\rho_0}\Pi_1+\frac{1}{\rho_0-\lambda^{(2)}}\Pi_2+\frac{1}{\rho_0-\lambda^{(3)}}\Pi_3\right]y, \tag{26}$$

where Π_i is the matrix associated with the orthogonal projection onto the eigenspace Γ_i, and the vector $y=G_1u_0$ is computed in (23). Since $q\in\Gamma_2$, the projections $P_1y=P_3y=0$, while $P_2y=y$. Using Lemma 1, we obtain

$$u_1=\frac{1}{\rho_0-\lambda^{(2)}}\sqrt{\frac{n-2}{n-1}}\gamma q=\frac{\sqrt{(n-2)(n-1)}}{\varepsilon\bar{a}n\left(1-\frac{m\bar{a}}{(n-1)}\right)}\gamma q, \tag{27}$$

which concludes the proof. □

We consolidate our claims in the following theorem, which is the main result of this paper.

Theorem 1. *Given a consensus protocol over an ADN with activity potentials given by* (2)*, $m \geq 1$, $\bar{a} > 0$, and $\varepsilon > 0$, the convergence factor is*

$$\begin{aligned} r &= 1 - \varepsilon \frac{2\bar{a}mn}{n-1} + \varepsilon^2 \bar{a} m \left[\frac{nm\bar{a}}{(n-1)^2} + m + 1 \right] \\ &\quad + \sigma^2 \frac{(n-2)m}{\bar{a}n\left(1 - \dfrac{m\bar{a}}{n-1}\right)} \gamma\beta + O(\sigma^3), \end{aligned} \tag{28}$$

where γ is defined in (22)*, and*

$$\beta := \frac{2n}{(n-1)^2}\varepsilon m\bar{a} - \frac{2n}{n-1} + \frac{n-1}{n-2}\varepsilon m - \frac{\varepsilon}{n-2}. \tag{29}$$

Proof. We compute the vector $z^T := u_0^T G_1$ as follows. First, we observe that $u_0^T(R \otimes R) = u_0^T$, since u_0 is an eigenvector associated with the eigenvalue 1 of the matrix $R \otimes R$. Then, $z^T = u_0^T M$ is computed by following the technique used in the proof of Lemma 3, whose details can be found in the Appendix. We report the final expression recalling the definition of q in (24), that is,

$$z = \sqrt{\frac{n-2}{n-1}}\varepsilon m\beta q, \tag{30}$$

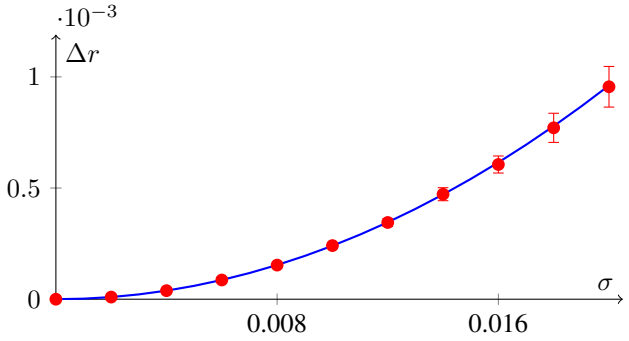
where β is defined in (29). Using Lemma 4 to evaluate u_1 and applying Proposition 4, we conclude that

$$\begin{aligned} \rho_2 &= \frac{\sqrt{(n-2)(n-1)}}{\varepsilon\bar{a}n\left(1 - \frac{m\bar{a}}{(n-1)}\right)} \gamma \sqrt{\frac{n-2}{n-1}} \varepsilon m\beta q^T q \\ &= \frac{(n-2)m}{\bar{a}n\left(1 - \frac{m\bar{a}}{n-1}\right)} \gamma\beta, \end{aligned} \tag{31}$$

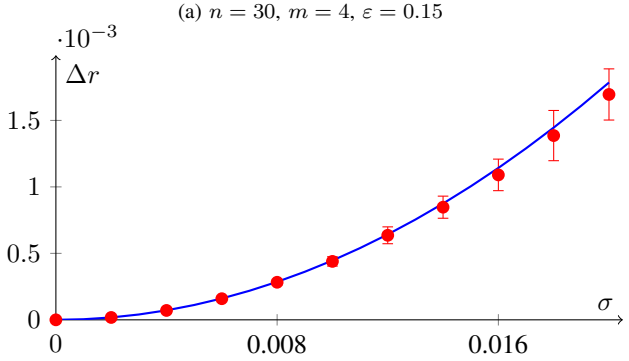
which yields the claim. □

The numerical estimations in Fig. 2 supports our analytical predictions and suggest that the accuracy of a parabolic representation for the convergence rate extends beyond the limit of small values of σ, upon which the perturbation analysis rests.

Remark 2. *The estimation in Theorem 1 can inform a qualitative analysis on the effect of the heterogeneity of the nodes' activity on the convergence factor of the consensus protocol. For $\sigma = 0$, the convergence rate is exactly given by the first three summands on the right hand side of* (28)*, analogously to the consensus protocol over conspecific agents considered in [24]. By introducing heterogeneity through the ADN paradigm, the convergence factor will vary, so that small values of σ will cause a change in the convergence factor of the order of σ^2. Whether this change will increase or decrease the value of r depends on the parameters of the ADN (that is, n, m, and $\bar{a}$) and the parameter ε of the consensus protocol. The scenario of large networks, with $n \to \infty$, will be extensively analyzed in Section V and explicit closed-form results are derived therein.*



(a) $n = 30$, $m = 4$, $\varepsilon = 0.15$



(b) $n = 50$, $m = 10$, $\varepsilon = 0.05$

Fig. 2: Variation of the convergence factor with respect to the case of nodes with the same activity, Δr, for increasing values of σ, for two choices of the model parameters (in both cases $\bar{a} = 0.1$). Vector h is generated uniformly at randomly under the constraints $\mathbb{1}^T h = 0$ and $||h|| = \sqrt{n}$. Consequently, the activity potential of node i is $a_i = \bar{a} + \sigma h_i$, for any $i \in \mathcal{V}$. Red circles are Monte Carlo estimations (over 100 realizations of h) with the corresponding 95% confidence intervals, and the blue curve is our analytical prediction, up to the second order power in σ.

B. Expected Consensus State

Assuming that $r < 1$, $x(k)$ converges almost surely to a consensus state $\bar{x}$. This state can be characterized through Proposition 3, leading to the following result.

Theorem 2. *Given a mean-square consentable protocol* (5) *over an ADN with activity potentials a_i, $i \in \mathcal{V}$, then $\lim_{k\to\infty} x(k) = \bar{x}\mathbb{1}$ almost surely, with*

$$\mathbb{E}[\bar{x}] = \pi^T x_0, \qquad \pi_i = \frac{a_i^{-1}}{\sum_{j\in\mathcal{V}} a_j^{-1}}. \tag{32}$$

Proof. By applying Proposition 3, we compute the left eigenvector of $\mathbb{E}[L]$ associated with the null eigenvalue. From the computations in Lemma 2, we recall that $\mathbb{E}[L] = \frac{n}{n-1}\text{diag}(a)R$. Observing that $\mathbb{1}^T R = 0$, we conclude

$$\pi^T \mathbb{E}[L] = 0 \iff \pi^T \text{diag}(a) \propto \mathbb{1}^T \iff \pi_i \propto a_i^{-1}. \tag{33}$$

The normalization of the eigenvector concludes the proof. □

Remark 3. *Consensus protocol over an ADN leads to a consensus state which is not the arithmetic average of the initial states. The initial condition of each node is weighted*

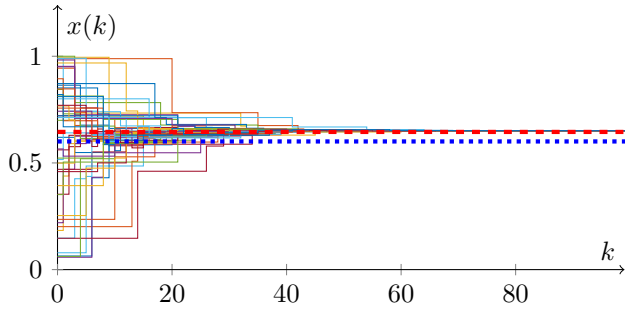


Fig. 3: Sample path of the process and compares the evolution of the state variables with the predicted consensus state (red dashed line). The arithmetic average of the initial conditions, which is the expected steady-state value for homogeneous systems, is shown as a blue dotted line. Numerical simulations are performed with $n = 50$, $\varepsilon = 0.05$, and $m = 10$. Following [26], activity potentials are distributed according to a rescaled power-law with exponent $\gamma = -2.2$ and a lower cutoff of $a_{\min} = 0.01$ to avoid singularities close to zero.

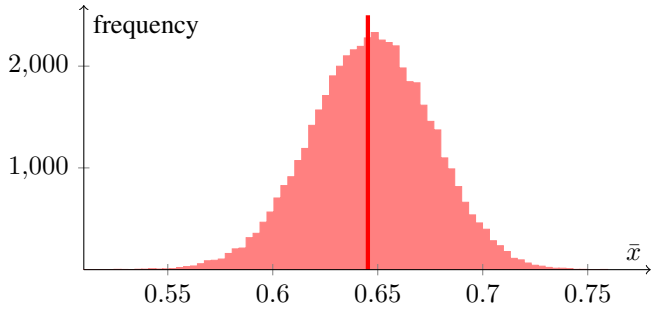


Fig. 4: Empirical distribution of the consensus values for set of Monte Carlo simulations over $50,000$ independent runs from the same initial condition of the state variables. The 95% confidence interval of the consensus state from Monte Carlo simulations is $[0.6448, 0.6454]$. The predicted consensus value from (32), $\mathbb{E}[\bar{x}] = 0.6453$, is plotted as a red line. Parameters are $n = 50$, $\varepsilon = 0.05$, and $m = 10$. Following [26], activity potentials are distributed according to a rescaled power-law with exponent $\gamma = -2.2$ and a lower cutoff of $a_{\min} = 0.01$ to avoid singularities close to zero.

by the inverse of its activity potential, which can be associated with its resistance to compromise. Nodes with low activity are less inclined to create connections, such that they will be less prone to compromise their state.

Figures 3 and 4 illustrates the outcome of numerical simulations that support our findings in Theorem 2. Figure 3 exemplifies a sample path of the consensus protocol, illustrating that the heterogeneity in the nodes' activity causes a shift of the consensus value away from the arithmetic average of initial conditions, which would be expected for a homogeneous systems. Figures 4 demonstrates results from Monte Carlo simulations that indicate very good agreement between the expected value of the empirical distribution and analytical predictions.

Remark 4. *Conducting a Taylor expansion on* (32) *with respect to σ, we discover that the consensus state is influenced by σ at the very first order, so that*

$$\begin{aligned}\mathbb{E}[\bar{x}] &= \frac{1}{n}\sum_{i\in\mathcal{V}} x_{0i} - \sigma\frac{1}{n\bar{a}}\sum_{i\in\mathcal{V}} h_i x_{0i} \\ &\quad +\sigma^2\frac{1}{n\bar{a}^2}\sum_{i\in\mathcal{V}}(h_i^2-1)x_{0i} + O(\sigma^3),\end{aligned} \tag{34}$$

where x_{0i} denotes the ith entry of the initial condition $x_0 \in \mathbb{R}^n$. For the problem analyzed in Fig. 3, the first-order approximation in (34) *would predict a consensus value of* 0.6505*, while retaining a parabolic expansion would yield* 0.6435*, with an error smaller than* 0.3%*.*

V. Application to Large Networks

We conclude this paper by performing an asymptotic analysis for large networks, in the limit $n \to \infty$. In this practically relevant case, numerical computation of the spectral radius of G in Proposition 2 would be unfeasible, strengthening the merit of our closed-form solution in Theorem 1 based on perturbation theory. In the homogeneous case of $\sigma = 0$, mean-square consentablility is attained for $\varepsilon(m+1) < 2$ and, given m and $\bar{a}$, $\varepsilon = \varepsilon^* = 1/(m+1)$ yields the fastest convergence rate [24]. In the presence of heterogeneity in the activity of the nodes, we obtain the following asymptotic expressions[1].

Corollary 1. *In the limit $n \to \infty$, the convergence factor of the consensus protocol* (5) *has the asymptotic expression:*

$$\begin{aligned}r &= 1 - 2\varepsilon\bar{a}m + \varepsilon^2\bar{a}m(m+1) \\ &\quad +\sigma^2\frac{m(2-\varepsilon(m+1))(2-\varepsilon m)}{\bar{a}} + O(\sigma^3).\end{aligned} \tag{35}$$

Proof. For large n, the prediction of Theorem 1 reduces to

$$r = 1 - 2\varepsilon\bar{a}m + \varepsilon^2\bar{a}m(m+1) + \sigma^2\frac{m}{\bar{a}}\gamma\beta + O(\sigma^3), \tag{36}$$

and the expressions for γ and β in (22) and (29), respectively, yield $\gamma = \varepsilon m + \varepsilon - 2$ and $\beta = \varepsilon m - 2$. The proof is completed by substituting these asymptotic expressions in (36). □

Remark 5. *Small heterogeneities have always a detrimental effect on the convergence factor. For $n \to \infty$, the coefficient of σ^2 in* (35) *is strictly positive for any choice of the parameters such that $\varepsilon(m+1) < 2$. Thus, heterogeinity in the nodes' activities decreases the convergence speed, potentially hindering consensus. Given $\varepsilon(m+1) < 2$, so that $r < 1$ when $\sigma = 0$, the largest level of heterogeneities that can be tolerated by the protocol before losing convergence can be estimated as $\sigma = \bar{a}\sqrt{\frac{\varepsilon}{2-\varepsilon m}}$. As one might anticipate, the critical value of σ scales with the average activity in the group, such that for ADNs with large values of $\bar{a}$, one may tolerate more severe heterogeneities. Interestingly, the larger is the value of ε, the more the protocol is sensitive to heterogeneities, since the nodes will tend to compromise more with their neighbors, thereby enhancing the overall effect of heterogeneities in the network. Finally, increasing m mitigates*

[1] Although $n \to \infty$, r is bounded since m is finite. In fact, a trivial bound on the spectral radius of matrix G can be obtained from (8), based on the fact that $\rho(L) \le ||L|| \le 2m$. Hence, $r \le (1+2\varepsilon m)^2$, for any value of n.

the effect of heterogenities, where the number of links created in each update is smaller.

Remark 6. *From* (35)*, we may seek to determine the fastest convergence rate that can be attained by the protocol on a given ADN and determine the value of ε that is conducive to optimal consensus. Toward this aim, we determine*

$$\varepsilon^* = \frac{1}{m+1} + \sigma^2 \frac{1}{\bar{a}^2} + O(\sigma^3), \tag{37}$$

which yields the optimal asymptotic convergence factor

$$r^* = \frac{1}{n+1} + \sigma^2 \frac{m(m+2)}{\bar{a}(m+1)} + O(\sigma^3). \tag{38}$$

Predictably, the fastest attainable rate of convergence decreases with σ^2.

Remark 7. *In the limit $n \to \infty$, one may offer a probabilistic interpretation of* (32)*. Specifically, let us assume that the initial conditions are drawn from a given scalar distribution X_0 and the activitiy potentials are also drawn from another, independent, distribution A, similar to the Monte Carlo simulations in Figs. 2, 3, and 4. Then, by the law of large numbers, the independence of the two distributions* (32) *from Theorem 2 reads*

$$\begin{aligned} \mathbb{E}[\bar{x}] &= \frac{\sum_{i\in\mathcal{V}} a_i^{-1} x_i}{\sum_{i\in\mathcal{V}} a_i^{-1}} = \frac{\mathbb{E}[A^{-1}X_0]}{\mathbb{E}[A^{-1}]} \\ &= \frac{\mathbb{E}[A^{-1}]\mathbb{E}[X_0]}{\mathbb{E}[A^{-1}]} = \mathbb{E}[X_0]. \end{aligned} \tag{39}$$

This asymptotic result indicates that, when initial conditions and activity potentials are independently distributed, the expected consensus state tends to the average of the initial conditions.

VI. Conclusion

In this paper, we have analytically studied a discrete-time consensus protocol over ADNs. The ADN paradigm constitutes a powerful viewpoint to examine dynamical systems in which the time-scales of network formation and the node dynamics are comparable. Using stochastic stability theory and eigenvalue perturbation analysis, we have established closed-form expressions for the rate of convergence to consensus and the expected consensus state, in terms of the distribution of the activity potentials in the network.

Our analytical results suggest that: i) even a modest amount of heterogeneity in the nodes' activity could affect the consensus protocol by slowing down convergence to the consensus state, and ii) nodes that are less active in generating connections dominate the consensus state of the network. Finally, we have focused on large networks, for which, in the absence of analytical results, the consensus dynamics is difficult to examine, because of its computational complexity. In this scenario, we derived the asymptotic expressions for the expected consensus state and for the convergence rate to consensus, demonstrating that heterogeneity is always detrimental to the coordination of large scale systems.

The main limitation of this study is the lack of an analytical bound for the accuracy of the estimations of the convergence rate and the expected consensus state. Such a limitation is inherent to perturbation theory that does not offer a direct way to estimate the residuals in the expansions. Our numerical simulations support that the perturbation analysis is valid for a relatively wide range of parameter values, whereby a parabolic dependence on the perturbation parameter is in excellent agreement with numerical simulations based on the complete ADN model.

In contrast with [36], our claims are not based on a time-scale separation between the network evolution and the nodes' dynamics. At each time step, we execute both the averaging process and the network formation, which co-evolve within a complex stochastic dynamics. The generality of the framework should be amenable for extension to nonlinear dynamics, critical to shedding light on synchronization phenomena [47]. A master stability function can be likely formulated by extending the line of arguments of [48] to tackle the role of heterogeneity on the linear stability of the synchronization manifold. Another avenue of future research is the study of real-world network features, such as a heterogeneous nodes attractiveness [30] and burstiness [35], toward the analysis of time-resolved datasets of socio-technical systems.

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APPENDIX

We present here the explicit computations of $\tilde{y}$. To keep the notation simple, all the summations are to be intended over the set of nodes $\mathcal{V}$, and $\sum_{k\neq i}$ means $\sum_{k\in\mathcal{V}\setminus\{i\}}$. When the summation is performed on the only index inside, we omit the summation index. We start by noticing that

$$\sum_{k\neq i} h_i = h_i \sum_{k\neq i} 1 = (n-1)h_i,$$

while

$$\sum_{k\neq i} h_k = \sum h_k - h_i = 0 - h_i = -h_i.$$

For the diagonal elements, we compute

$$\begin{aligned}
\tilde{y}_i^i = & \sum_{h,k\in\mathcal{V}} M_{ik}^{ih}(u_0)_{kh} = \frac{1}{\sqrt{n-1}} \sum_{h,k\in\mathcal{V}} M_{ik}^{ih} R_{kh} = \\
= & \frac{1}{\sqrt{n-1}} \left[\frac{n-1}{n} \sum_{h\in\mathcal{V}} M_{ih}^{ih} - \frac{1}{n} \sum_{h\in\mathcal{V},k\neq h} M_{ik}^{ih} \right] = \\
= & \frac{1}{\sqrt{n-1}} \left[\frac{n-1}{n} \left(M_{ii}^{ii} + \sum_{h\neq i} M_{ih}^{ih} \right) \right. \\
& \left. -\frac{1}{n} \left(\sum_{k\neq i} M_{ik}^{ii} + \sum_{h\neq i} M_{ii}^{ih} + \sum_{h\neq i} \sum_{k\neq i,h} M_{ik}^{ih} \right) \right] \\
= & \frac{1}{\sqrt{n-1}} \left[\frac{n-1}{n} \left(\varepsilon m h_i(\varepsilon m - 2) + \varepsilon^2 \frac{m}{n-1} \sum_{h\neq i} h_i \right) \right. \\
& -\frac{1}{n} \left(-\varepsilon \frac{m}{n-1} (\varepsilon m - 1) \sum_{k\neq i} h_i - \varepsilon \frac{m}{n-1} (\varepsilon m - 1) \cdot \right. \\
& \left. \left. \cdot \sum_{h\neq i} h_i + \varepsilon^2 \frac{m(m-1)}{(n-1)(n-2)} \sum_{h\neq i} \sum_{k\neq i,h} h_i \right) \right] \\
= & \frac{\varepsilon m h_i}{n\sqrt{n-1}} \left[(n-1)(\varepsilon m - 1) + 2(\varepsilon m - 1) - \varepsilon(m-1) \right] \\
= & \frac{1}{\sqrt{n-1}} \varepsilon m h_i (\varepsilon m - 2 + \varepsilon),
\end{aligned}$$

while, following a similar argument, off-diagonal elements are

$$\begin{aligned}
\tilde{y}_i^j = & \frac{1}{\sqrt{n-1}}\left[\frac{n-1}{n}\left(M_{ii}^{ji}+M_{ii}^{jj}+\sum_{h\neq i,j}M_{ih}^{jh}\right)\right.\\
& \left.-\frac{1}{n}\left(M_{ii}^{jj}+\sum_{h\neq j}M_{ii}^{jh}+\sum_{k\neq i}M_{ik}^{jj}+\sum_{h\neq j}\sum_{k\neq i,j}M_{ik}^{jh}\right)\right]\\
= & \frac{1}{\sqrt{n-1}}\left[\frac{n-1}{n}\left(-\varepsilon\frac{m}{n-1}[\varepsilon m\bar{a}(h_i+h_j)-h_j]\right)\right.\\
& -\varepsilon\frac{m}{n-1}[\varepsilon m\bar{a}(h_i+h_j)-h_i]+\varepsilon^2\frac{m^2}{(n-1)^2}\cdot\\
& \left.\cdot\sum_{h\neq i,j}(h_i+h_j)\right)-\frac{1}{n}\left(\varepsilon m(h_i+h_j)(\varepsilon m\bar{a}-1)\right.\\
& -\varepsilon\frac{m}{n-1}\sum_{h\neq j}[\varepsilon m\bar{a}(h_i+h_j)-h_j]\\
& -\varepsilon\frac{m}{n-1}\sum_{k\neq i}[\varepsilon m\bar{a}(h_i+h_j)-h_i]\\
& \left.+\varepsilon^2\frac{m^2}{(n-1)^2}\bar{a}\sum_{h\neq j}\sum_{k\neq i,j}(h_i+h_j)\right)\Bigg]\\
= & \frac{1}{\sqrt{n-1}}\varepsilon m(h_i+h_j)\frac{1}{n-1}\left(-\frac{n}{n-1}\varepsilon m\bar{a}+1\right).
\end{aligned}$$

Now, we introduce

$$\alpha := (\varepsilon m-2+\varepsilon),\quad \beta := \frac{1}{n-1}\left(-\frac{n}{n-1}\varepsilon m\bar{a}+1\right),$$

so that

$$\bar{y}_i^i = \frac{1}{\sqrt{n-1}}\varepsilon m\alpha h_i,\quad \bar{y}_i^j = \frac{1}{\sqrt{n-1}}\varepsilon m\beta(h_i+h_j).$$

With this notation, we compute

$$\begin{aligned}
y_i^i = & \frac{(n-1)^2}{n^2}\tilde{y}_i^i-\frac{n-1}{n^2}\left(\sum_{h\neq i}\tilde{y}_i^h+\sum_{k\neq i}\tilde{y}_k^i\right)+\frac{1}{n^2}\sum_{h,k\neq i}\tilde{y}_k^h\\
= & \varepsilon m\frac{1}{\sqrt{n-1}}\left[\frac{(n-1)^2}{n^2}\alpha h_i-\frac{n-1}{n^2}\beta\sum_{h\neq i}(h_i+h_h)\right.\\
& -\frac{n-1}{n^2}\beta\sum_{k\neq i}(h_k+h_i)+\frac{1}{n^2}\beta\sum_{h\neq i}\sum_{k\neq i,h}(h_h+h_k)\\
& \left.+\frac{1}{n^2}\alpha\sum h_h\right]\\
= & \varepsilon m\frac{1}{\sqrt{n-1}}\left[\frac{(n-1)^2}{n^2}\alpha h_i-2\frac{(n-1)^2}{n^2}\beta h_i\right.\\
& +2\frac{n-1}{n^2}\beta h_i+\frac{1}{n^2}\beta\big(-(n-2)h_i+\sum_{h\neq i}(-h_i-h_h)\big)\\
& \left.-\frac{1}{n^2}\alpha h_i\right]\\
= & \varepsilon m\frac{1}{\sqrt{n-1}}\left[\frac{n-2}{n}\alpha h_i-2\frac{(n-1)(n-2)}{n^2}\beta h_i\right.\\
& \left.+\frac{2(n-2)}{n^2}\beta h_i\right]\\
= & \varepsilon m\frac{1}{\sqrt{n-1}}\left(\frac{n-2}{n}\alpha-2\frac{n-2}{n}\beta\right)h_i\\
= & \varepsilon m\frac{1}{\sqrt{n-1}}\frac{n-2}{n}(\alpha-2\beta)h_i;
\end{aligned}$$

and

$$\begin{aligned}
y_i^j = & \varepsilon m\frac{1}{\sqrt{n-1}}\left[\frac{(n-1)^2}{n^2}\beta(h_i+h_j)-\frac{n-1}{n^2}\alpha h_i\right.\\
& -\frac{n-1}{n^2}\beta\sum_{h\neq i,h}(h_i+h_h)-\frac{n-1}{n^2}\alpha h_j\\
& -\frac{n-1}{n^2}\beta\sum_{k\neq i,h}(h_k+h_j)+\frac{1}{n^2}\alpha\sum_{h\neq i,j}h_h\\
& \left.+\frac{1}{n^2}\beta\sum_{n\neq j}\sum_{k\neq i,h}h_k+\frac{1}{n^2}\beta\sum_{h\neq k}\sum_{k\neq i,h}h_h\right]\\
= & \varepsilon m\frac{1}{\sqrt{n-1}}\left[\frac{(n-1)^2}{n^2}\beta(h_i+h_j)\right.\\
& -\frac{n-1}{n^2}\alpha(h_i+h_j)+\frac{n-1}{n^2}\beta(h_i+h_j)\\
& +\frac{n-1}{n^2}\beta(h_i+h_j)-\frac{1}{n^2}\alpha(h_i+h_j)\\
& \left.-\beta\frac{n-2}{n^2}h_j-\beta\frac{n-1}{n^2}h_i+\frac{1}{n^2}\beta h_j\right]\\
= & \varepsilon m\frac{1}{\sqrt{n-1}}\left(-\frac{1}{n}\alpha+\frac{2}{n}\beta\right)\\
= & -\varepsilon m\frac{1}{n\sqrt{n-1}}(\alpha-2\beta).
\end{aligned}$$

Finally, introducing $\gamma := \alpha-2\beta$ we obtain the expression for y in (23).